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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/724,586A

DATE: 09/16/2003

TIME: 16:00:02

Input Set : A:\04871~1.txt

Output Set: N:\CRF4\09162003\I724586A.raw

3 <110> APPLICANT: Sakowicz, Roman  
 4 Goldstein, Lawrence  
 6 <120> TITLE OF INVENTION: Identification and Expression of Novel Kinesin Motor Protein  
 8 <130> FILE REFERENCE: UCSD-04871  
 10 <140> CURRENT APPLICATION NUMBER: 09/724,586A  
 11 <141> CURRENT FILING DATE: 2000-11-28  
 13 <160> NUMBER OF SEQ ID NOS: 9  
 15 <170> SOFTWARE: PatentIn version 3.2  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 784  
 19 <212> TYPE: PRT  
 20 <213> ORGANISM: Thermomyces lanuginosus  
 23 <220> FEATURE:  
 24 <221> NAME/KEY: MISC\_FEATURE  
 25 <223> OTHER INFORMATION: TL-gamma ATP-dependent plus end-directed microtubule motor  
 26 protein  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: DOMAIN  
 30 <222> LOCATION: (1)..(357)  
 31 <223> OTHER INFORMATION: kinesin-like microtubule motor domain  
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 34 <221> NAME/KEY: DOMAIN  
 35 <222> LOCATION: (358)..(442)  
 36 <223> OTHER INFORMATION: neck domain links motor domain to stalk domain  
 38 <220> FEATURE:  
 39 <221> NAME/KEY: DOMAIN  
 40 <222> LOCATION: (602)..(784)  
 41 <223> OTHER INFORMATION: tail domain  
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 46 1 5 10 15  
 49 Asn Ala Arg Glu Ile Asp Arg Gly Ala Lys Cys Ile Val Arg Met Glu  
 50 20 25 30  
 53 Gly Asn Gln Thr Ile Leu Thr Pro Pro Pro Gly Ala Glu Glu Lys Ala  
 54 35 40 45  
 57 Arg Lys Ser Gly Lys Thr Ile Met Asp Gly Pro Lys Ala Phe Ala Phe  
 58 50 55 60  
 61 Asp Arg Ser Tyr Trp Ser Phe Asp Lys Asn Ala Pro Asn Tyr Ala Arg  
 62 65 70 75 80  
 65 Gln Glu Asp Leu Phe Gln Asp Leu Gly Val Pro Leu Leu Asp Asn Ala  
 66 85 90 95  
 69 Phe Lys Gly Tyr Asn Asn Cys Ile Phe Ala Tyr Gly Gln Thr Gly Ser  
 70 100 105 110

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73 Gly Lys Ser Tyr Ser Met Met Gly Tyr Gly Lys Glu His Gly Val Ile
74      115          120          125
77 Pro Arg Ile Cys Gln Asp Met Phe Arg Arg Ile Asn Glu Leu Gln Lys
78      130          135          140
81 Asp Lys Asn Leu Thr Cys Thr Val Glu Val Ser Tyr Leu Glu Ile Tyr
82 145          150          155          160
85 Asn Glu Arg Val Arg Asp Leu Leu Asn Pro Ser Thr Lys Gly Asn Leu
86          165          170          175
89 Lys Val Arg Glu His Pro Ser Thr Gly Pro Tyr Val Glu Asp Leu Ala
90          180          185          190
93 Lys Leu Val Val Arg Ser Phe Gln Glu Ile Glu Asn Leu Met Asp Glu
94          195          200          205
97 Gly Asn Lys Ala Arg Thr Val Ala Ala Thr Asn Met Asn Glu Thr Ser
98      210          215          220
101 Ser Arg Ser His Ala Val Phe Thr Leu Thr Leu Thr Gln Lys Trp His
102 225          230          235          240
105 Asp Glu Glu Thr Lys Met Asp Thr Glu Lys Val Ala Lys Ile Ser Leu
106          245          250          255
109 Val Asp Leu Ala Gly Ser Glu Arg Ala Thr Ser Thr Gly Ala Thr Gly
110          260          265          270
113 Ala Arg Leu Lys Glu Gly Ala Glu Ile Asn Arg Ser Leu Ser Thr Leu
114          275          280          285
117 Gly Arg Val Ile Ala Ala Leu Ala Asp Met Ser Ser Gly Lys Gln Lys
118          290          295          300
121 Lys Asn Gln Leu Val Pro Tyr Arg Asp Ser Val Leu Thr Trp Leu Leu
122 305          310          315          320
125 Lys Asp Ser Leu Gly Gly Asn Ser Met Thr Ala Met Ile Ala Ala Ile
126          325          330          335
129 Ser Pro Ala Asp Ile Asn Phe Glu Glu Thr Leu Ser Thr Leu Arg Tyr
130          340          345          350
133 Ala Asp Ser Ala Lys Arg Ile Lys Asn His Ala Val Val Asn Glu Asp
134          355          360          365
137 Pro Asn Ala Arg Met Ile Arg Glu Leu Lys Glu Glu Leu Ala Gln Leu
138          370          375          380
141 Arg Ser Lys Leu Gln Ser Ser Gly Gly Gly Gly Gly Ala Gly Gly
142 385          390          395          400
145 Ser Gly Gly Pro Val Glu Glu Ser Tyr Pro Pro Asp Thr Pro Leu Glu
146          405          410          415
149 Lys Gln Ile Val Ser Ile Gln Gln Pro Asp Ala Thr Val Lys Lys Met
150          420          425          430
153 Ser Lys Ala Glu Ile Val Glu Gln Leu Asn Gln Ser Glu Lys Leu Tyr
154          435          440          445
157 Arg Asp Leu Asn Gln Thr Trp Glu Glu Lys Leu Ala Lys Thr Glu Glu
158          450          455          460
161 Ile His Lys Glu Arg Glu Ala Ala Leu Glu Glu Leu Gly Ile Ser Ile
162 465          470          475          480
165 Glu Lys Gly Phe Val Gly Pro Tyr His Ser Lys Glu Met Pro His Leu
166          485          490          495
169 Val Asn Leu Ser Asp Asp Pro Leu Leu Ala Glu Cys Leu Val Tyr Asn

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170	500	505	510	
173	Ile Lys Pro Gly Gln Thr Arg Val Gly Asn Val Asn Gln Asp Thr Gln			
174	515	520	525	
177	Ala Glu Ile Arg Leu Asn Gly Ser Lys Ile Leu Lys Glu His Cys Thr			
178	530	535	540	
181	Phe Glu Asn Val Asp Asn Val Val Thr Ile Val Pro Asn Glu Lys Ala			
182	545	550	555	560
185	Ala Val Met Val Asn Gly Val Arg Ile Asp Lys Pro Thr Arg Leu Arg			
186	565	570	575	
189	Ser Gly Tyr Arg Ile Ile Leu Gly Asp Phe His Ile Phe Arg Phe Asn			
190	580	585	590	
193	His Pro Glu Glu Ala Arg Ala Glu Arg Gln Glu Gln Ser Leu Leu Arg			
194	595	600	605	
197	His Ser Val Thr Asn Ser Gln Leu Gly Ser Pro Ala Pro Gly Arg His			
198	610	615	620	
201	Asp Arg Thr Leu Ser Lys Ala Gly Ser Asp Ala Asp Gly Asp Ser Arg			
202	625	630	635	640
205	Ser Asp Ser Pro Leu Pro His Phe Arg Gly Lys Asp Ser Asp Trp Phe			
206	645	650	655	
209	Tyr Ala Arg Arg Glu Ala Ala Ser Ala Ile Leu Gly Leu Asp Gln Lys			
210	660	665	670	
213	Ile Ser His Leu Thr Asp Asp Glu Leu Asp Ala Leu Phe Asp Asp Val			
214	675	680	685	
217	Gln Lys Ala Arg Ala Val Arg Arg Gly Leu Val Glu Asp Asn Glu Asp			
218	690	695	700	
221	Ser Asp Ser Gln Ser Ser Phe Pro Val Arg Asp Lys Tyr Met Ser Asn			
222	705	710	715	720
225	Gly Thr Ile Asp Asn Phe Ser Leu Asp Thr Ala Ile Thr Met Pro Gly			
226	725	730	735	
229	Thr Pro Arg Ser Asp Asp Asp Gly Asp Ala Leu Phe Phe Gly Asp Lys			
230	740	745	750	
233	Lys Ser Lys Gln Asp Ala Ser Asn Val Asp Val Glu Glu Leu Arg Gln			
234	755	760	765	
237	Gln Gln Ala Gln Met Glu Glu Ala Leu Lys Thr Ala Lys Gln Glu Phe			
238	770	775	780	
241	<210> SEQ ID NO: 2			
242	<211> LENGTH: 2352			
243	<212> TYPE: DNA			
244	<213> ORGANISM: Thermomyces lanuginosus			
247	<220> FEATURE:			
248	<221> NAME/KEY: misc_feature			
249	<223> OTHER INFORMATION: TL-gamma ATP-dependent plus end-directed microtubule motor			
250	protein			
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257	cctccgggtt ccgaagagaa ggccgttaaa agtgccaaaa ctattatggta tggccgaaag	180		
259	gcatttgcgt tcgatcggtc gtattggtcc tttgacaaga atgctccaa ctatgcgaga	240		
261	caggaagacc tattccaaga tctcgagtc ccgcttctgg ataatgcatt caagggttat	300		

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263	aacaattgtatcttcgccta	cggtcagacc	ggttcgccga	agtccatttc	aatgatgggc	360
265	tatggcaagg	agcatggcgt	gatcccgcgg	atttgccagg	acatgttccg	420
267	gaactgcaga	aggacaagaa	cctcacttgc	accgtcgaag	tttcgtactt	480
269	aatgaacgag	tgcgagactt	gctgaatccg	tcgacacaagg	ggaatctcaa	540
271	cacccgtcga	ccggcccccta	cgtggaggac	ttggcgaagc	tggcgtgcg	600
273	gaaatcgaaa	atctcatgga	tgagggcaac	aaagccagaa	cggttgcgc	660
275	aacgagacat	ccagtcgatc	ccacgcgcgtc	ttcactttga	ccttgcgcga	720
277	gatgaagaga	ccaaaatgga	cacagagaag	gttgcgaaga	tcagtcgtgt	780
279	ggttctgagc	gagcaacgtc	cacccggagct	actggagcgc	gactgaagga	840
281	atcaaccgct	cactttcgac	ccttaggtcgt	gtgattgcag	cgctagcgg	900
283	gaaaaacaga	agaagaatca	gttagtacct	taccgagatt	cggtactgac	960
285	aaggactcct	ttggaggcaa	ctcgatgacc	gccatgatttgc	ccgccatttc	1020
287	attaactttg	aagagactct	cagtaccctt	cgatatgcgg	actctgcgaa	1080
289	aaccacgcag	tggtaaatga	agacccgaac	gcccggatga	tccgcgagtt	1140
291	ctcgcgcagc	tgaggagcaa	actccagagc	agtggtggag	gtggagggtgg	1200
293	tctggcgggc	cagtggagga	atcgatcccg	cccgacacgc	cgctcgagaa	1260
295	tcgattcagc	agccggatgc	gacagtcaag	aaaatgagca	aggcagaaat	1320
297	ctgaaccaga	gtgagaagct	ctatcgggat	ctcaatcaga	cctggaaaga	1380
299	aagaccgagg	aaatccacaa	ggaacgagaa	gcccgcctcg	aggagctggg	1440
301	aaaaagggtt	ttgttggccc	ttaccactcc	aaagaaatgc	cacatctagt	1500
303	gatgatcctc	ttctggctga	gtgtcttgc	tacaacatca	agcccgcc	1560
305	gaaaaacgtca	accaagatac	acaagcggaa	attcgctga	acggttcgaa	1620
307	gaacactgtatcttcgccta	cggtcagacc	ggttcgccga	agtccatttc	aatgatgggc	1680
309	<210>	SEQ ID NO: 3	<211>	LENGTH: 21	<212>	TYPE: DNA
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315	ccaggccgtc	acgaccggac	actgagcaag	gcccggatcc	atgcggacgg	1860
317	tcagattctc	ctttgccgca	ctttcgtgga	aaggatagcg	cgatgttcta	1920
319	gaagctgcta	gcccgcgtt	agggttggat	cagaagatct	tgctcgcagg	1980
321	ttggatgcat	tatggacga	tggtcgaaaa	gcccggcc	ctcatctgac	2040
323	gacaacgaag	atagcgattc	gcagagttcg	tttccggatcc	agatgacgag	2100
325	ggaaccattt	ataatttctc	gctcgatacc	gccattacta	tgccggatcc	2160
327	gatgacgacg	gtgacgcgt	gttttttgtt	gataagaagt	ccctcgatgt	2220
329	gttgcgttt	aggagttgcg	tcaacagcag	gctcagatgg	cgaaacagga	2280
331	aagcaggaat	tc				2340
334						2352
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**PATENT APPLICATION:** US/09/724,586A TIME: 16:00:02

Input Set : A:\04871~1.txt  
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354 <400> SEQUENCE: 4	
355 gaattcctgc ttcgctgttt tca	23
358 <210> SEQ ID NO: 5	
359 <211> LENGTH: 30	
360 <212> TYPE: DNA	
361 <213> ORGANISM: Artificial Sequence	
363 <220> FEATURE:	
364 <223> OTHER INFORMATION: Synthetic	
367 <220> FEATURE:	
368 <221> NAME/KEY: misc_feature	
369 <222> LOCATION: (25)..(25)	
370 <223> OTHER INFORMATION: n is a, c, g, or t	
372 <400> SEQUENCE: 5	
<b>W--&gt; 373 ggcggatcc atytygcht ayggncarac</b>	<b>30</b>
376 <210> SEQ ID NO: 6	
377 <211> LENGTH: 30	
378 <212> TYPE: DNA	
379 <213> ORGANISM: Artificial Sequence	
381 <220> FEATURE:	
382 <223> OTHER INFORMATION: Synthetic	
385 <220> FEATURE:	
386 <221> NAME/KEY: misc_feature	
387 <222> LOCATION: (16)..(16)	
388 <223> OTHER INFORMATION: n is a, c, g, or t	
390 <220> FEATURE:	
391 <221> NAME/KEY: misc_feature	
392 <222> LOCATION: (28)..(28)	
393 <223> OTHER INFORMATION: n is a, c, g, or t	
395 <400> SEQUENCE: 6	
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399 <210> SEQ ID NO: 7	
400 <211> LENGTH: 30	
401 <212> TYPE: DNA	
402 <213> ORGANISM: Artificial Sequence	
404 <220> FEATURE:	
405 <223> OTHER INFORMATION: Synthetic	
408 <220> FEATURE:	
409 <221> NAME/KEY: misc_feature	
410 <222> LOCATION: (16)..(16)	
411 <223> OTHER INFORMATION: n is a, c, g, or t	
413 <220> FEATURE:	
414 <221> NAME/KEY: misc_feature	
415 <222> LOCATION: (28)..(28)	
416 <223> OTHER INFORMATION: n is a, c, g, or t	
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422 <210> SEQ ID NO: 8	
423 <211> LENGTH: 21	
424 <212> TYPE: DNA	

RAW SEQUENCE LISTING ERROR SUMMARY                   DATE: 09/16/2003  
PATENT APPLICATION: US/09/724,586A               TIME: 16:00:03

Input Set : A:\04871~1.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 25  
Seq#:6; N Pos. 16,28  
Seq#:7; N Pos. 16,28